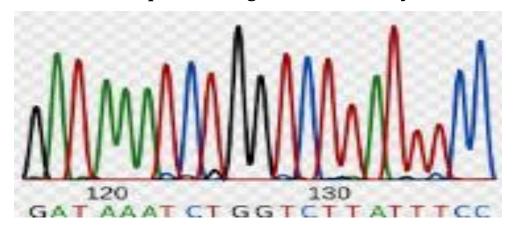


SANT BABA BHAG SINGH UNIVERSITY, JALANDHAR

Value ADDED Course

DNA Sequences: Alignments and Analysis



Department of Botany (UISH)

DURRATION: 30Hours

COORDINATOR

Dr Anil Kumar Singh
Assistant Professor (Botany)
Department of Agriculture and Botany
University Institute of Sciences & Humanities
Sant Baba Bhag Singh University, Jalandhar

REGISTRATION FORM

Value Added Course on "DNA Sequences: Alignments and Analysis"

Name		
Father Name		
Mother Name		
Date of birth	Department	
Class/Semester		
Address for correspondence_		
Contact No.		
Email		
Signature of Applicant		Date

VENUE

Block No.5, Room No. 513, Sant Baba Bhag Singh University, Jalandhar, Punjab, India.

For more Information Contact

Dr Anil Kumar Singh Assistant Professor Department of Agriculture and Botany University institute of Sciences & Humanities Sant Baba Bhag Singh University, Jalandhar-144030

Title of Value Added Course: DNA Sequences: Alignments and Analysis

Value added courses are the types of courses which help a particular individual to develop their skills in their chosen field of the study. The Value Added Courses aim to provide additional learner centric graded skill oriented technical training, with the primary objective of improving the employability skills of students. It is important for all institutions to supplement the curriculum to make students better prepared to meet industry demands as well as develop their own interests and aptitudes.

Course Name	Course Code	Duration	Batch Timings	Tentative Batch Start Date	Course Coordinator
DNA Sequences: Alignments and Analysis	BOT011	30 hrs	12:30 – 1:20pm 3:30 – 4:20pm (tentative to be adjusted as per time table)	October 2020	Dr. Anil Kumar Singh

Eligibility:

Final year graduate students and Master students

Prerequisites

Basic knowledge in life sciences

Course Fee:

Applicable /Not Applicable

Course Duration information:

30 hrs.

Course Syllabus

Week 1:

Biological Data Acquisition: The form of biological information. Retrieval methods for DNA sequence. Databases— Format and Annotation: Conventions for database indexing and specification of search terms, Common sequence file formats, Annotated sequence databases - primary sequence databases, Organism specific databases.

Data – Access, Retrieval and Submission: Standard search engines; Data retrieval tools, Submission of (new and revised) data; Sequence Similarity Searches: Local versus global.

Week 2:

Distance metrics: Similarity and homology Scoring matrices. Dynamic programming algorithms, Needleman-wunsch and Smith-waterman, Heuristic Methods of sequence alignment, FASTA, BLAST and PSI BLAST, Multiple Sequence Alignment and software tools for pairwise and multiple sequence alignment.

Genome Analysis: Whole genome analysis, existing software tools; Genome Annotation (link is external) and Gene Prediction; ORF finding.

Phylogenetic Analysis: Comparative genomics, orthologs, paralogs. Methods of phylogenetic analysis: UPGMA, WPGMA, neighbour joining method, Fitch/Margoliash method, Character Based Methods.

Course Outcome:

A student completing DNA Sequences: Alignments and Analysis shall be able to apply knowledge to understand features, function, structure, or evolution of genome.